

B. In the Drawings

Please approve the corrections to the drawings, as indicated on the attached "Letter to the Examiner Requesting Approval of Changes to the Drawings."

II. REMARKS

A. Introduction

In this Office Action, claims 24-26, 28-31, 39 and 40 are noted as allowed.

In summary of this Response, the specification is amended, a new "Sequence Listing" is submitted, so that each sequence is identified, and a "Statement Regarding Sequence Listing" is submitted.

III. CONCLUSION

In light of the above amendments and remarks, it is respectfully submitted that the application is now in condition for allowance.

If there are any additional fees associated with this Response, please charge same to our Deposit Account No. 19-3935.

Finally, if there are any formal matters remaining after this Response, the undersigned would appreciate a telephone conference with the Examiner to attend to these matters.

Respectfully submitted,

STAAS & HALSEY LLP

Date: 5/9/03

By:   
William F. Herbert  
Registration No. 31,024

700 Eleventh Street, NW, Suite 500  
Washington, D.C. 20001  
(202) 434-1500

**VERSION WITH MARKINGS TO SHOW CHANGES MADE -  
37 C.F.R. §121(b) and/or (c)**

**IN THE WRITTEN DESCRIPTION**

Please AMEND the Written Description as follows.

On page 4, the first full paragraph, please amend as follows.

A DNA normally exists in a double-stranded state as two complementary and anisotropic base sequences. In the two base sequences, the facing bases have a fixed relationship, and the adenine A faces the thymine T, while the guanine G faces the cytosine C. An example of a DNA double-strand is shown as follows:

5' end ATGCATGCTAGCTAGCT 3' end (strand A) (SEQUENCE ID NO. 1)

||||| ||||| ||||| |||||

3' end TACGTACGATCGATCGA 5'end (strand B) (SEQUENCE ID NO. 2)

← : →

On page 4, second full paragraph, please amend as follows:

Strand B is complementary to strand A and is represented as a single strand as follows:

5' end AGCTAGCTAGCATGCAT 3' end (strand B) (SEQUENCE ID NO. 3).

→

On page 41, first full paragraph, please amend as follows:

Then, in step S62, when the vector data base includes base sequences outside the multiple cloning site, a sequence containing the base sequence and the 5' side residual multiple cloning site 5MCS is defined as a side residual vector area 5VA.

That is, when five base sequences are included to the 5' side of the 5' side retrieval key as shown in FIG. 17 (in this example, to the 5' side of the 5' side residual multiple cloning site), the five bases to the 5' side of the 5MCS are added to the 5MCS in defining the 5' side residual vector area 5VA in step S62. In FIG. 17, the 5VA is the base sequence GTGCCAAGCTT (SEQUENCE ID NO. 4). If only the base sequence in the multiple cloning site is included in the vector data base, then the 5VA is assumed to equal the 5MCS. However, since the data base normally includes the base sequences before and after the multiple cloning site, the homology check is effective as described below.